#5

FIG. 1

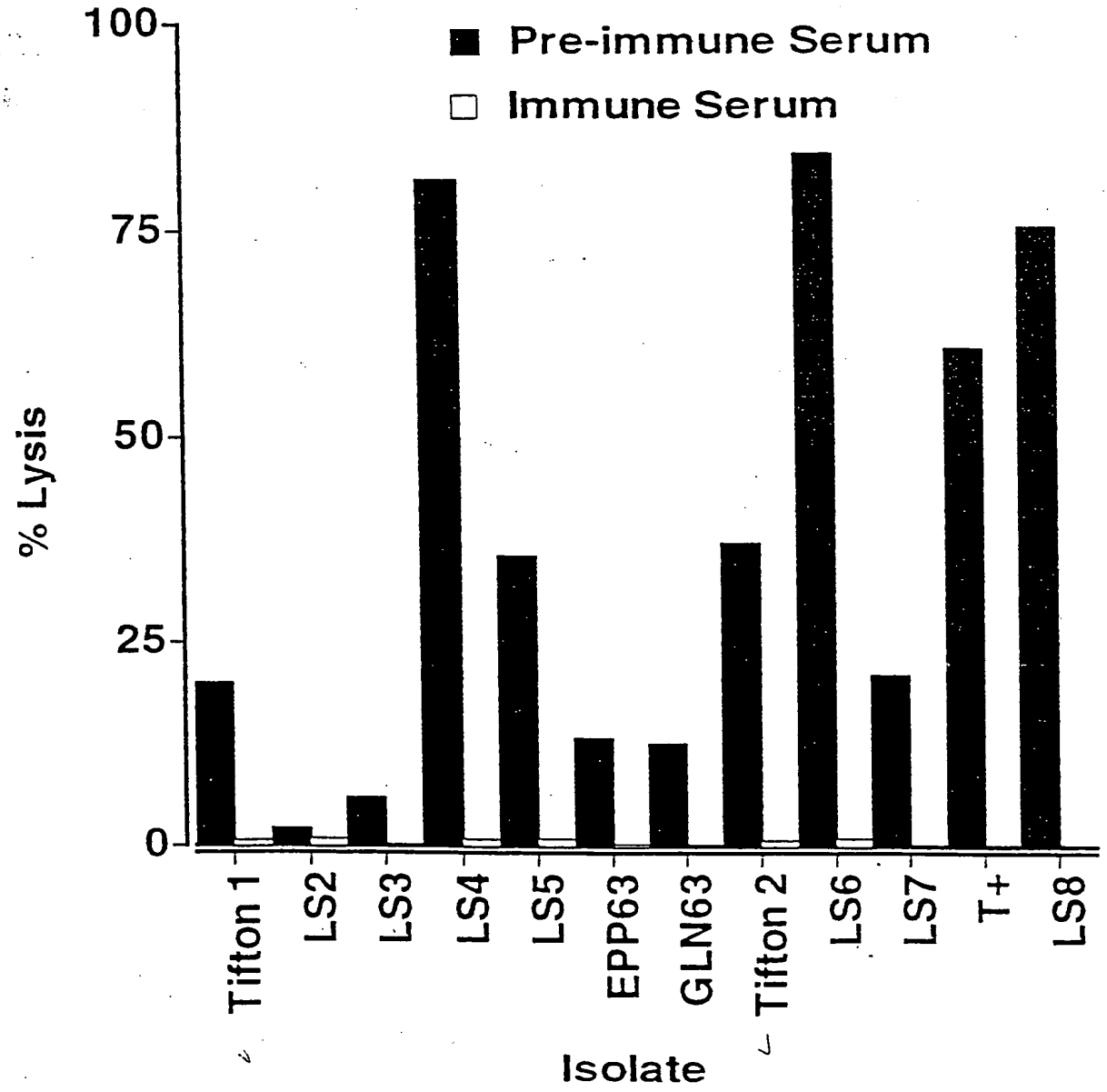


FIG. 2

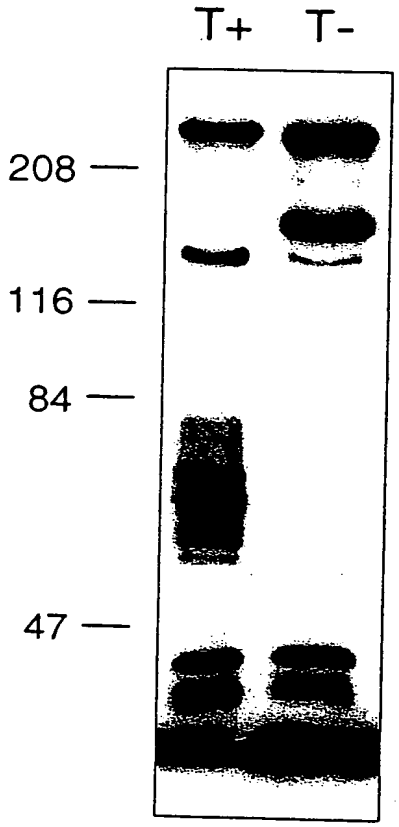


FIG 3-1

Appendix A update-July 1999

Bases 1-1200
Amino acids 1-400

```
   1 ATGTCCAATATAAATGTAATTAAATCTAATATTCAAGCAGGCTTGAATTCAACAAAGTCT    60
   1  M  S  N  I  N  V  I  K  S  N  I  Q  A  G  L  N  S  T  K  S    20

  61 GGATTAAAAAATCTTTACTTGGCTATTCCCAAAGATTATGATCCGCAAAAAGGTGGGACT   120
  21  G  L  K  N  L  Y  L  A  I  P  K  D  Y  D  P  Q  K  G  G  T    40

 121 TTAAATGATTTTATTAAAGCTGCTGATGAATTAGGTATTGCTCGTTTAGCAGAAGAGCCT   180
  41  L  N  D  F  I  K  A  A  D  E  L  G  I  A  R  L  A  E  E  P    60

 181 AATCACACTGAAACAGCAAAAAAATCTGTTGACACAGTAAATCAGTTTCTCTCTCTCACA   240
  61  N  H  T  E  T  A  K  K  S  V  D  T  V  N  Q  F  L  S  L  T    80

 241 CAAACTGGTATTGCTATTTCTGCAACAAAATTAGAAAAGTTCTTACAAAAACATTCTACC   300
  81  Q  T  G  I  A  I  S  A  T  K  L  E  K  F  L  Q  K  H  S  T   100

 301 AATAAGTTAGCCAAAGGGTTAGACAGTGTAGAAAATATTGATCGTAAATTAGGTAAAGCA   360
 101  N  K  L  A  K  G  L  D  S  V  E  N  I  D  R  K  L  G  K  A   120

 361 AGTAATGTATTATCAACATTAAGCTCTTTTTTGGGCACTGCATTAGCGGGTATAGAACTT   420
 121  S  N  V  L  S  T  L  S  S  F  L  G  T  A  L  A  G  I  E  L   140

 421 GATTCTTTAATCAAAAAAGGTGATGCTGCACCTGATGCTTTGGCTAAAGCTAGTATTGAC   480
 141  D  S  L  I  K  K  G  D  A  A  P  D  A  L  A  K  A  S  I  D   160

 481 TTGATTAATGAGATAATTGGTAATCTATCTCAGAGTACTCAAACGATTGAAGCATTTTCT   540
 161  L  I  N  E  I  I  G  N  L  S  Q  S  T  Q  T  I  E  A  F  S   180

 541 TCACAGTTAGCAAAGTTAGGTTCTACTATATCGCAGGCTAAAGGCTTCTCTAATATAGGA   600
 181  S  Q  L  A  K  L  G  S  T  I  S  Q  A  K  G  F  S  N  I  G   200

 601 AACAAGTTGCAAAACTTAAATTTTTCTAAAACAAATCTTGGTTTGGAAATAATTACTGGT   660
 201  N  K  L  Q  N  L  N  F  S  K  T  N  L  G  L  E  I  I  T  G   220

 661 TTGCTATCAGGCATTTCTGCAGGCTTTGCTTTAGCGGATAAAAATGCATCGACTGGCAAA   720
 221  L  L  S  G  I  S  A  G  F  A  L  A  D  K  N  A  S  T  G  K   240

 721 AAAGTTGCTGCAGGTTTTGAATTAAGCAATCAAGTTATTGGTAATGTAACAAAAGCAATT   780
 241  K  V  A  A  G  F  E  L  S  N  Q  V  I  G  N  V  T  K  A  I   260

 781 TCTTCATATGTTTTAGCACAACGTGTTGCTGCTGGTCTATCAACTACTGGTGCTGTTGCT   840
 261  S  S  Y  V  L  A  Q  R  V  A  A  G  L  S  T  T  G  A  V  A   280

 841 GCTTTAATTACTTCATCGATTATGTTGGCAATTAGTCCTTTGGCATTTATGAATGCAGCA   900
 281  A  L  I  T  S  S  I  M  L  A  I  S  P  L  A  F  M  N  A  A   300

 901 GATAAATTCAATCATGCTAATGCTCTTGATGAGTTTGCAAAACAATTCCGAAAATTTGGC   960
 301  D  K  F  N  H  A  N  A  L  D  E  F  A  K  Q  F  R  K  F  G   320

 961 TATGATGGGGATCATTTATTGGCTGAATATCAGCGTGGTGTGGGTACTATTGAAGCTTCA  1020
 321  Y  D  G  D  H  L  L  A  E  Y  Q  R  G  V  G  T  I  E  A  S   340

1021 TTAACTACAATTAGTACGGCATTAGGTGCAGTTTCTGCTGGTGTTTCCGCTGCTGCTGTA  1080
 341  L  T  T  I  S  T  A  L  G  A  V  S  A  G  V  S  A  A  A  V   360

1081 GGATCTGCTGTTGGTGCACCGATTGCACTATTAGTTGCAGGTGTTACAGGATTGATCTCT  1140
 361  G  S  A  V  G  A  P  I  A  L  L  V  A  G  V  T  G  L  I  S   380

1141 GGAATTTTAGAAGCGTCTAAACAGGCAATGTTTGAAAGTGTTGCTAACCGTTTACAAGGT  1200
 381  G  I  L  E  A  S  K  Q  A  M  F  E  S  V  A  N  R  L  Q  G   400
```

FIG 3-2

Appendix A update-July 1999, continued

Bases 1201-2400
Amino acids 401-800

```
1201 AAAATTTTAGAGTGGGAAAAGCAAAATGGCGGTCAGAACTATTTTGATAAAGGCTATGAT   1260
 401  K  I  L  E  W  E  K  Q  N  G  G  Q  N  Y  F  D  K  G  Y  D    420

1261 TCTCGTTATGCTGCTTATTTAGCTAATAACTTAAAATTTTTGTCTGAGCTAAATAAAGAG   1320
 421  S  R  Y  A  A  Y  L  A  N  N  L  K  F  L  S  E  L  N  K  E    440

1321 TTGGAAGCTGAACGTGTTATTGCAATCACCCAACAACGTTGGGATAATAATATTGGTGAG   1380
 441  L  E  A  E  R  V  I  A  I  T  Q  Q  R  W  D  N  N  I  G  E    460

1381 TTAGCAGGTATTACCAAATTGGGTGAACGCATTAAGAGCGGAAAAGCTTATGCAGATGCT   1440
 461  L  A  G  I  T  K  L  G  E  R  I  K  S  G  K  A  Y  A  D  A    480

1441 TTTGAAGATGGCAAGAAAGTTGAAGCTGGTTCCAATATTACTTTGGATGCTAAAACTGGT   1500
 481  F  E  D  G  K  K  V  E  A  G  S  N  I  T  L  D  A  K  T  G    500

1501 ATCATAGACATTAGTAATTCAAATGGGAAAAAAACGCAAGCGTTGCATTTCACTTCGCCT   1560
 501  I  I  D  I  S  N  S  N  G  K  K  T  Q  A  L  H  F  T  S  P    520

1561 TTGTTAACAGCAGGAACTGAATCACGTGAACGTTTAACTAATGGTAAATACTCTTATATT   1620
 521  L  L  T  A  G  T  E  S  R  E  R  L  T  N  G  K  Y  S  Y  I    540

1621 AATAAGTTAAAATTCGGACGTGTAAAAAACTGGCAAGTTACAGATGGAGAGGCTAGTTCT   1680
 541  N  K  L  K  F  G  R  V  K  N  W  Q  V  T  D  G  E  A  S  S    560

1681 AAATTAGATTTCTCTAAAGTTATTCAGCGTGTAGCCGAGACAGAAGGCACAGACGAGATT   1740
 561  K  L  D  F  S  K  V  I  Q  R  V  A  E  T  E  G  T  D  E  I    580

1741 GGTCTAATAGTAAATGCAAAAGCTGGCAATGACGATATCTTTGTTGGTCAAGGTAAAATG   1800
 581  G  L  I  V  N  A  K  A  G  N  D  D  I  F  V  G  Q  G  K  M    600

1801 AATATTGATGGTGGAGATGGACACGATCGTGTCTTCTATAGTAAAGACGGAGGATTTGGT   1860
 601  N  I  D  G  G  D  G  H  D  R  V  F  Y  S  K  D  G  G  F  G    620

1861 AATATTACTGTAGATGGTACGAGTGCAACAGAAGCAGGCAGTTATACAGTTAATCGTAAG   1920
 621  N  I  T  V  D  G  T  S  A  T  E  A  G  S  Y  T  V  N  R  K    640

1921 GTTGCTCGAGGTGATATCTACCATGAAGTTGTGAAGCGTCAAGAAACCAAGGTGGGTAAA   1980
 641  V  A  R  G  D  I  Y  H  E  V  V  K  R  Q  E  T  K  V  G  K    660

1981 CGTACTGAAACTATCCAGTATCGTGATTATGAATTAAGAAAAGTTGGGTATGGTTATCAG   2040
 661  R  T  E  T  I  Q  Y  R  D  Y  E  L  R  K  V  G  Y  G  Y  Q    680

2041 TCTACCGATAATTTGAAATCAGTAGAAGAAGTAATTGGTTCTCAATTTAATGATGTATTC   2100
 681  S  T  D  N  L  K  S  V  E  E  V  I  G  S  Q  F  N  D  V  F    700

2101 AAAGGTTCTAAATTCAACGACATATTCCATAGTGGTGAAGGTGATGATTTACTCGATGGT   2160
 701  K  G  S  K  F  N  D  I  F  H  S  G  E  G  D  D  L  L  D  G    720

2161 GGTGCTGGTGACGACCGCTTGTTTGGTGGTAAAGGCAACGATCGACTTTCTGGAGATGAA   2220
 721  G  A  G  D  D  R  L  F  G  G  K  G  N  D  R  L  S  G  D  E    740

2221 GGCGATGATTTACTCGATGGCGGTTCTGGTGATGATGTATTAAATGGTGGTGCTGGTAAT   2280
 741  G  D  D  L  L  D  G  G  S  G  D  D  V  L  N  G  G  A  G  N    760

2281 GATGTCTATATCTTTCGGAAAGGTGATGGTAATGATACTTTGTACGATGGCACGGGCAAT   2340
 761  D  V  Y  I  F  R  K  G  D  G  N  D  T  L  Y  D  G  T  G  N    780

2341 GATAAATTAGCATTTGCAGATGCAAATATATCTGATATTATGATTGAACGTACCAAAGAG   2400
 781  D  K  L  A  F  A  D  A  N  I  S  D  I  M  I  E  R  T  K  E    800
```

FIG 3-3

Appendix A update-July 1999, continued

Bases 2401-2784
Amino acids 801-927

```
2401 GGTATTATAGTTAAACGAAATGATCATTCAGGTAGTATTAACATACCAAGATGGTACATA   2460
 801  G  I  I  V  K  R  N  D  H  S  G  S  I  N  I  P  R  W  Y  I    820

2461 ACATCAAATTTACAAAATTATCAAAGTAATAAAACAGATCATAAAATTGAGCAACTAATT   2520
 821  T  S  N  L  Q  N  Y  Q  S  N  K  T  D  H  K  I  E  Q  L  I    840

2521 GGTAAAGATGGTAGTTATATCACTTCCGATCAAATTGATAAAATTTTGCAAGATAAGAAA   2580
 841  G  K  D  G  S  Y  I  T  S  D  Q  I  D  K  I  L  Q  D  K  K    860

2581 GATGGTACAGTAATTACATCTCAAGAATTGAAAAAGCTTGCTGATGAGAATAAGAGCCAA   2640
 861  D  G  T  V  I  T  S  Q  E  L  K  K  L  A  D  E  N  K  S  Q    880

2641 AAATTATCTGCTTCGGACATTGCAAGTAGCTTAAATAAGCTAGTTGGGTCAATGGCACTA   2700
 881  K  L  S  A  S  D  I  A  S  S  L  N  K  L  V  G  S  M  A  L    900

2701 TTTGGTACAGCAAATAGTGTGAGTTCTAACGCCTTACAGCCAATTACACAACCAACTCAA   2760
 901  F  G  T  A  N  S  V  S  S  N  A  L  Q  P  I  T  Q  P  T  Q    920

2761 GGAATTTTGGCTCCAAGTGTTTAG          SEQ ID NO: 1                 2784
 921  G  I  L  A  P  S  V  *           SEQ ID NO: 2                  928
```

FIG. 4

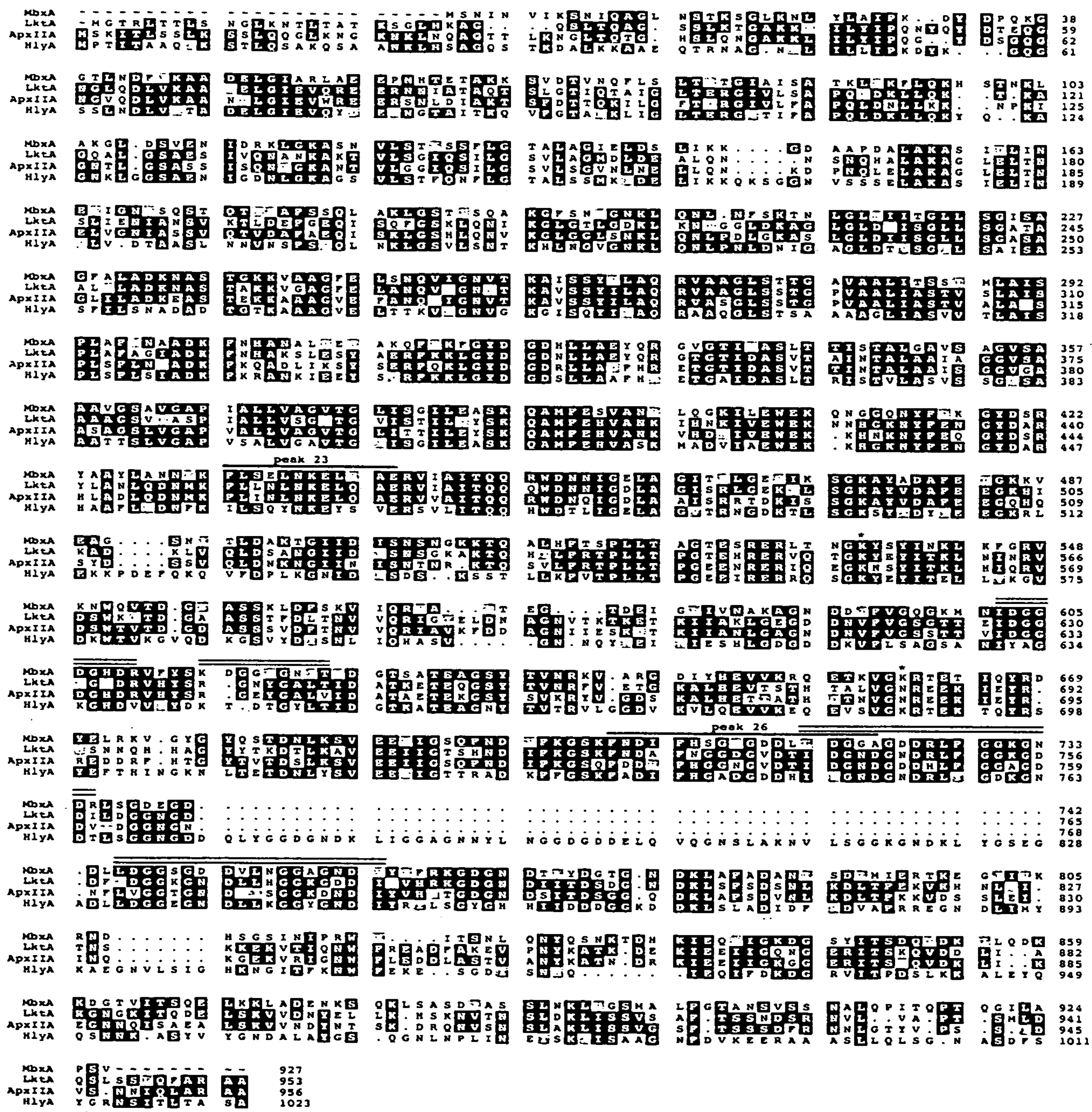


FIG.5

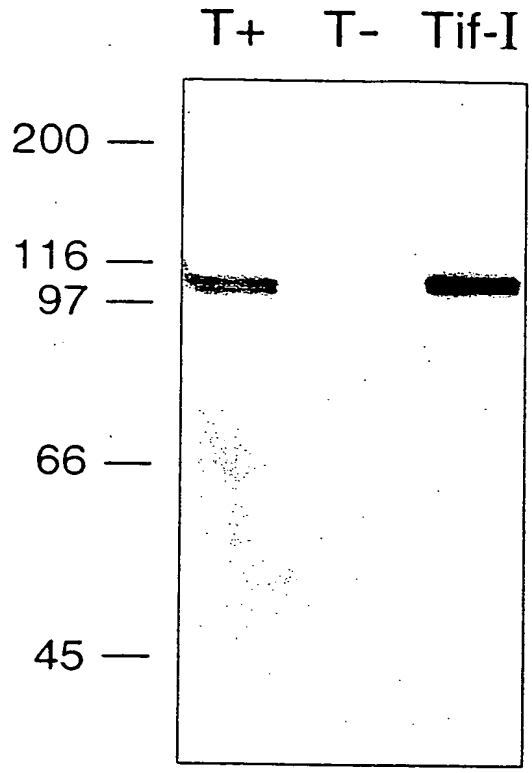


FIG.6

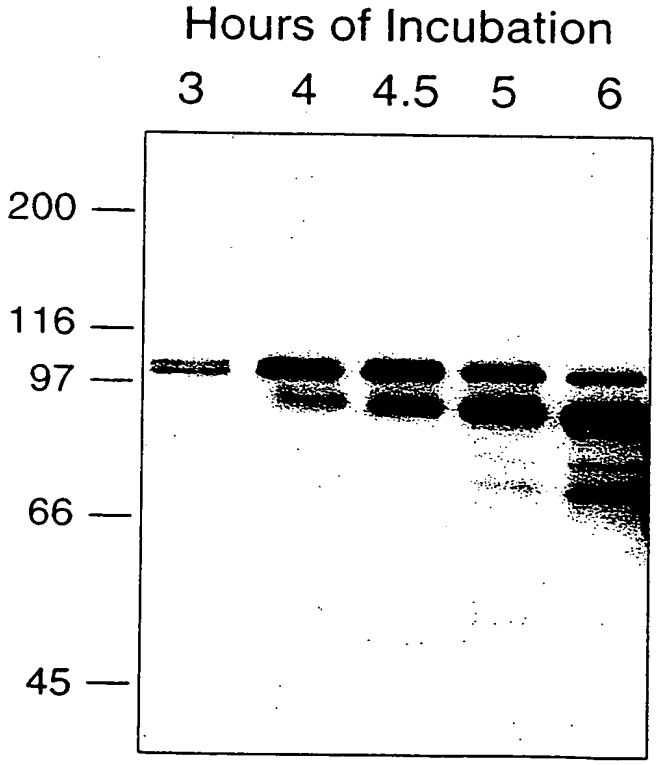
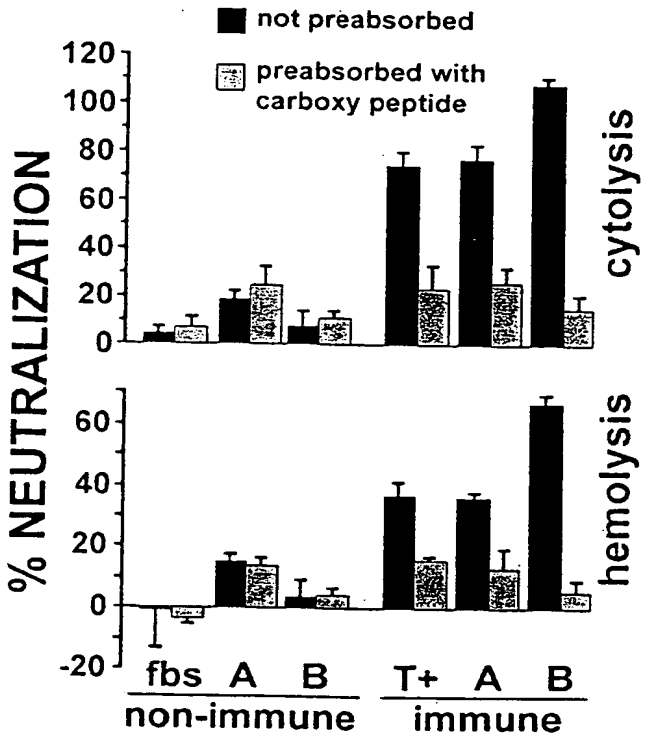


FIG. 7


not preabsorbed
preabsorbed with carboxy peptide
% NEUTRALIZATION
120
100
80
60
40
20
0
cytolysis
60
40
20
0
-20
hemolysis
fbs
A
B
T+
A
B
non-immune
immune

8-1

mbxB

mbx

```
   1 ATGGGTGGTGATACTTCTTTAATTAGACTTAATTTACAAACCCTTAATAGTAATTTAGTT    60
   1  M  G  G  D  T  S  L  I  R     N  L  Q  T  L  N  S  N  L  V

  61 ATGATAGATTATGCTCAACAACCTGCTCTATCTGCTCTGGTTATCCTTGCCAAATACTAT   120
  21  M  I  D  Y  A  Q  Q  P  A  L  S  A  L  V  I  L  A  K  Y  Y    40

 121 GGTATTTCTGCAAGTCCAGCAGACATTATGCATCAGTTTTCTGATAATACAAAAGGAGAC   180
  41  G  I  S  A  S  P  A  D  I  M  H  Q  F  S  D  N  T  K  G  D    60

 181 CTGAATGAAATTGAATGGATGTTGGCAGCAAAGAAATTAGAATTAAAGGTAAAGATTATA   240
  61  L  N  E  I  E  W  M  L  A  A  K  K  L  E  L  K  V  K  I  I    80

 241 AAACAGCCTTTAACTCGATTGTCAATGATAACACTTCCTGCTTTGGTGTGGTGTGATAAT   300
  81  K  Q  P  L  T  R  L  S  M  I  T  L  P  A  L  V  W  C  D  N   100

 301 AAGCCCGATTTAGATCAAAATTTAAACTCTCATTTTATACTAACTAAAATTGATGGGGTG   360
 101  K  P  D  L  D  Q  N  L  N  S  H  F  I  L  T  K  I  D  G  V   120

 361 GGATCTGCTGCAAAATATCTCATCTACGATTTGATTGAGAATCGTCCCATAATATTAGAT   420
 121  G  S  A  A  K  Y  L  I  Y  D  L  I  E  N  R  P  I  I  L  D   140

 421 GCAAGTGAGTTTTCTGAAAGATATTCTGGTAAGTTAATGCTAGTAACTTCCCGTGCGTCA   480
 141  A  S  E  F  S  E  R  Y  S  G  K  L  M  L  V  T  S  R  A  S   160

 481 ATATTGGGTTCATTGGCTAAATTTGATTTTACTTGGTTTATTCCTGCGGTAATCAAATAT   540
 161  I  L  G  S  L  A  K  F  D  F  T  W  F  I  P  A  V  I  K  Y   180

 541 CGTTATATTTTTTTTGAAGTCATCGTTATTTCAGTGGTGCTACAGATTTTTGCTCTGATT   600
 181  R  Y  I  F  F  E  V  I  V  I  S  V  V  L  Q  I  F  A  L  I   200

 601 ACGCCATTGTTTTTTCAGGTTGTGATGGATAAGGTATTGGTGCATCGTGGTTTTTCTACT   660
 201  T  P  L  F  F  Q  V  V  M  D  K  V  L  V  H  R  G  F  S  T   220

 661 CTGGATGTGGTAGCGATTGCCTTGTTGGTAGTAAGTTTATTTGAAGTCATTTTAAGTGGT   720
 221  L  D  V  V  A  I  A  L  L  V  V  S  L  F  E  V  I  L  S  G   240

 721 CTACGCACTTATATTTTTGCTCATACAACCTCTCGAATTGATGTAGAGCTAGGAGCACGA   780
 241  L  R  T  Y  I  F  A  H  T  T  S  R  I  D  V  E  L  G  A  R   260

 781 TTATTTCGTCATCTATTAGCTCTACCGCTTGCTTATTTTGAGAGTAGAAGAGTAGGCGAT   840
 261  L  F  R  H  L  L  A  L  P  L  A  Y  F  E  S  R  R  V  G  D   280

 841 ACAGTTGCACGTATACGTGAATTGGAACATATCCGCAATTTCTTAACTGGTCAAGCTCTC   900
 281  T  V  A  R  I  R  E  L  E  H  I  R  N  F  L  T  G  Q  A  L   300

 901 ACTTCAGTTTTAGATTTGGTGTTTTCTTTTATATTCTTGTTTGTAATGTGGTATTACAGC   960
 301  T  S  V  L  D  L  V  F  S  F  I  F  L  F  V  M  W  Y  Y  S   320

 961 CCTACTTTAACACTGGTAGTTTTGGCATCATTACCAATATATGCGTTTTGGTCTGCCTTT  1020
 321  P  T  L  T  L  V  V  L  A  S  L  P  I  Y  A  F  W  S  A  F   340

1021 ATTAGCCCAATTTTACGCACTCGACTAAATGATCAATTTGCACGCAATGCAGATAATCAA  1080
 341  I  S  P  I  L  R  T  R  L  N  D  Q  F  A  R  N  A  D  N  Q   360

1081 TCTTTTTTAGTGGAAAGTATTACTGCGGTTGGTACGGTAAAAGCAATGGCAGTTGAACCT  1140
 361  S  F  L  V  E  S  I  T  A  V  G  T  V  K  A  M  A  V  E  P   380

1141 CAAATGACCCGTCGCTGGGATAATCAATTAGCAGCTTATGTGGTTTCTAGTTTTCGGGTA  1200
 381  Q  M  T  R  R  W  D  N  Q  L  A  A  Y  V  V  S  S  F  R  V   400

1201 GCTAAGTTGGCAATGGTTGGGCAGCAAGGAGTACAACTCATTCAAAAGATGGTTATTGTG  1260
 401  A  K  L  A  M  V  G  Q  Q  G  V  Q  L  I  Q  K  M  V  I  V   420

1261 GCAACTCTATGGATTGGTGCAAAATTGGTAATTGAAGGCAAGCTATCGGTAGGTCAATTA  1320
 421  A  T  L  W  I  G  A  K  L  V  I  E  G  K  L  S  V  G  Q  L   440
```

```
1321 ATAGCATTTAATATGCTGGCAGGTCAGGTGGCCGCTCCTGTTATCCGCCTGGCACAGCTA   1380
 441  I  A  F  N  M  L  A  G  Q     A  A  P  V  I  R  L  A  Q  L

1381 TGGCAAGATTTTCAGCAAGTAGGTATTTCAGTGGCGAGATTGGGTGATATTTTAAATACT   1440
 461  W  Q  D  F  Q  Q  V  G  I  S  V  A  R  L  G  D  I  L  N  T    480

1441 CCAACTGAGCATTCTACATCTCGCTTAACTTTACCTGATATTAAGGGTGATATTACATTT   1500
 481  P  T  E  H  S  T  S  R  L  T  L  P  D  I  K  G  D  I  T  F    500

1501 GAAAATGTTGATTTTCGCTACAAAATAGATGGGCATTTAATATTACAGAATTTAAATTTA   1560
 501  E  N  V  D  F  R  Y  K  I  D  G  H  L  I  L  Q  N  L  N  L    520

1561 CAGATTAACGCTGGAGAGATACTAGGTATCGTAGGACGCTCTGGTTCAGGTAAATCAACA   1620
 521  Q  I  N  A  G  E  I  L  G  I  V  G  R  S  G  S  G  K  S  T    540

1621 TTGACAAAATTAGTACAGCGTTTATATGTACCAGAAAATGGGCGAATATTAGTTGATGGA   1680
 541  L  T  K  L  V  Q  R  L  Y  V  P  E  N  G  R  I  L  V  D  G    560

1681 AACGATTTGGCATTAGCTGATCCCGCTTGGCTGCGTCGCCAAGTGGGTGTTGTTTTGCAG   1740
 561  N  D  L  A  L  A  D  P  A  W  L  R  R  Q  V  G  V  V  L  Q    580

1741 GAAAATGTGTTACTCAATCGTAGTATTCGAGATAATATTGCCCTAACTGATACGGGCATG   1800
 581  E  N  V  L  L  N  R  S  I  R  D  N  I  A  L  T  D  T  G  M    600

1801 TCATTAGAGTTTATTATCCAGGCTGCCAAGATGTCTGGGGCACATGACTTTATTATGGAA   1860
 601  S  L  E  F  I  I  Q  A  A  K  M  S  G  A  H  D  F  I  M  E    620

1861 TTGCCTGAGGGTTATGATACGATTGTTGGAGAGCAAGGTGCAGGCTTGTCAGGTGGACAA   1920
 621  L  P  E  G  Y  D  T  I  V  G  E  Q  G  A  G  L  S  G  G  Q    640

1921 CGCCAGCGTATCGCTATTGCGCGTGCTTTAATTACCAATCCGCGTATTTTGATTTTTGAT   1980
 641  R  Q  R  I  A  I  A  R  A  L  I  T  N  P  R  I  L  I  F  D    660

1981 GAAGCTACTAGTGCATTAGACTATGAGTCGGAAAGGGCTATTATGCAAAATATGCAGGCA   2040
 661  E  A  T  S  A  L  D  Y  E  S  E  R  A  I  M  Q  N  M  Q  A    680

2041 ATTTGCCAAGGTAGAACAGTGTTGATTATTGCACATCGCTTATCTACCGTAAAAATGGCA   2100
 681  I  C  Q  G  R  T  V  L  I  I  A  H  R  L  S  T  V  K  M  A    700

2101 CATCGCATTATTGCAATGGACAAGGGGAAAATTGTAGAGCAAGGCACACATCAAGAATTG   2160
 701  H  R  I  I  A  M  D  K  G  K  I  V  E  Q  G  T  H  Q  E  L    720

2161 TTGCAAAAAGAAGATGGTTACTATCGTTATTTATATGATTTGCAGAATGGATAAA        2215
 721  L  Q  K  E  D  G  Y  Y  R  Y  L  Y  D  L  Q  N  G  *          739
```

FIG. 8-2

FIG. 9

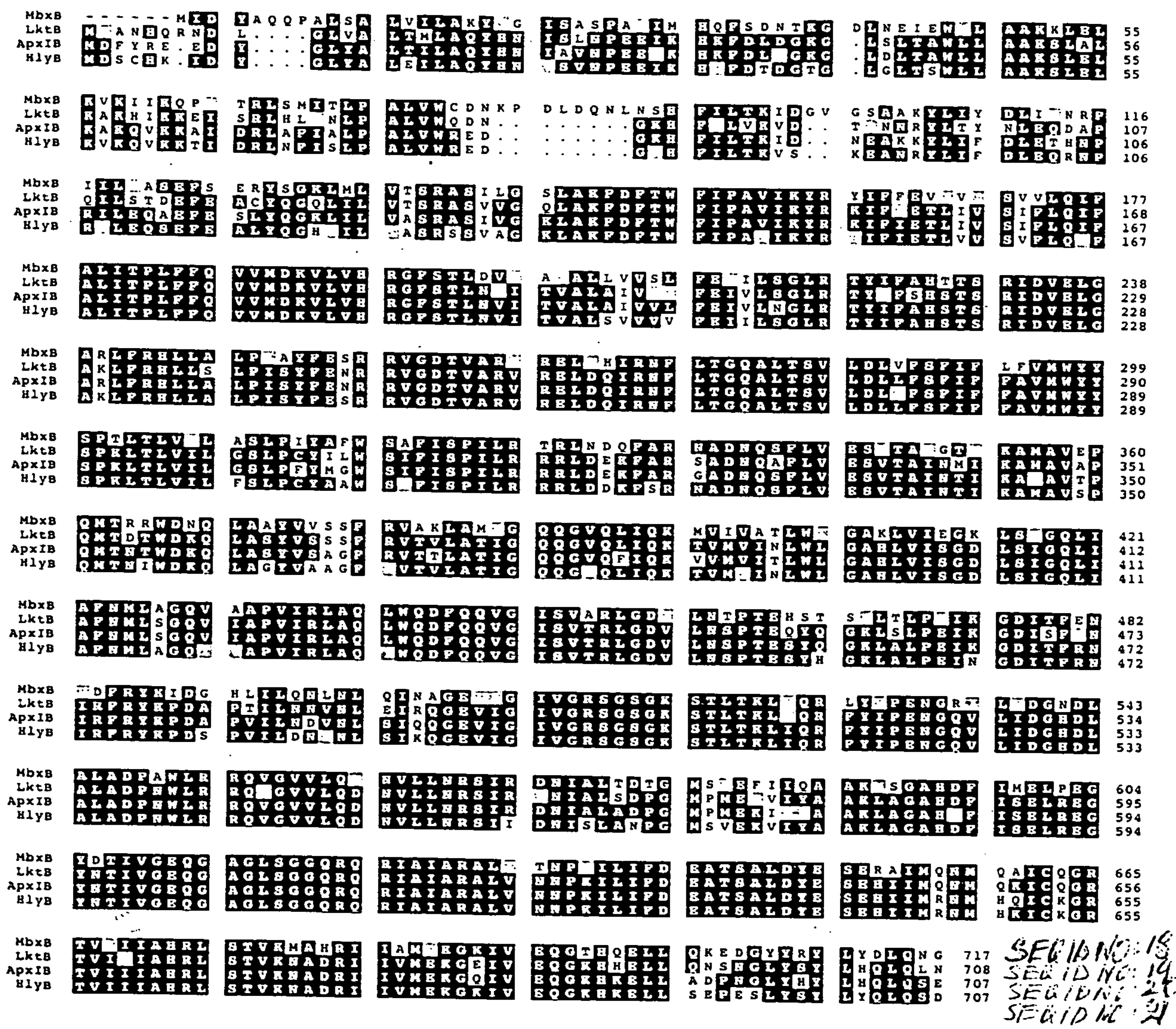


FIG. 10

```
DNASIS  Translation Editor [11-00 C gene.dna]
       1 ATGACGAAAAAGTTTGCAGAGCTAGGTTTAATTGCATGGCTTTGGTCTAACTCTGATATG     60
         1  M  T  K  K  F  A  E  L  G  L  I  A  W  L  W  S  N  S  D  M     20

      61 CATAAACATTGGACGTTGTCTTTGTTTGCGACCAATGTTATTCCGGCAATTGAGACAGGT    120
        21  H  K  H  W  T  L  S  L  F  A  T  N  V  I  P  A  I  E  T  G     40

     121 CAATATGTTATATTGAAAAGAGAAGATATGCCTGTAGCATATTGTAGTTGGGCTAAACTT    180
        41  Q  Y  V  I  L  K  R  E  D  M  P  V  A  Y  C  S  W  A  K  L     60

     181 AGTTTAGAAAACGAGGTTAAATATATTAACGATGTTACTTCTCTTAAGTTAGATGACTGG    240
        61  S  L  E  N  E  V  K  Y  I  N  D  V  T  S  L  K  L  D  D  W     80

     241 CAGTCAGGTGACCGAAACTGGTTTATTGACTGGATTGCTCCATTTGGCGATAGTCTTACA    300
        81  Q  S  G  D  R  N  W  F  I  D  W  I  A  P  F  G  D  S  L  T    100

     301 CTCACAAAACACATGAGAACGTTATTTTCAGATGAATTGTTTAGAGCGATTCGTGTAGAT    360
       101  L  T  K  H  M  R  T  L  F  S  D  E  L  F  R  A  I  R  V  D    120

     361 GGAAATTCATCGCATGGTAAGATATCTGAATTTTATGGAAAGTCTGTTGATTCAAAATTA    420
       121  G  N  S  S  H  G  K  I  S  E  F  Y  G  K  S  V  D  S  K  L    140

     421 GCCTCAAGAATATTTGCACAATATCACGAAGATTTGACGAGCAAATTGTCAACTCAGAAT    480
       141  A  S  R  I  F  A  Q  Y  H  E  D  L  T  S  K  L  S  T  Q  N    160

     481 AATTTTATTATATCTAAAGATAATTAA                                     507
       161  N  F  I  I  S  K  D  N  *                                     169
```

mbxC

MbxC

FIG. 11

MbxC	---MTKKFAE	LGLIAWLWSN	SD[illegible]HKHWTLS	LFATNVIPAI	ETGQY	42
LktC	--MNQSYFNL	LGNITWLWMN	SSLHKEWSCE	LLARNVIPAI	ENEQY	43
ApxIC	MSKKINGFEV	LGEVAWLWAS	SPLHRKWPLS	LLAINVLPAI	ESNQY	45
HlyC	-MNRNNPLEV	LGHVSWLWAS	SPLHRNWPVS	LFAINVLPAI	RANQY	44
MbxC	V[illegible]LKR[illegible]DMPV	AYCSWAKLSL	ENEVKYINDV	TSLKLDDWQS	GDRNW	87
LktC	MLLIDNGIPI	AYCSWADLNL	ETEVKYIKD[illegible]	NSLTPE[illegible]WQS	GDRRW	88
ApxIC	VLLKRDGFPI	A[illegible]CSWANLNL	ENEIKYLDDV	ASLVADDWTS	GDRRW	90
HlyC	ALLTRDNYPV	AYCSWANLSL	ENEIKYLNDV	TSLVAEDWTS	GDR[illegible]W	89
MbxC	FIDWIAPFGD	SLTLTKHMRT	LFSDELFRAI	RVDGNSS.HG	KISEF	131
LktC	IIDW[illegible]APFGH	SQLLYKKMCQ	K[illegible]PDM[illegible]VRSI	RFYPKQKELG	KIAYF	133
ApxIC	FIDWIAPFGD	SAALYKHMRD	NFPNELFRAI	RVDPDSR.VG	KISEF	134
HlyC	FIVWIAPFGD	NGALYK[illegible]MRK	KFPDELFRAI	RVDPKTH.VG	K[illegible]SEF	133
MbxC	[illegible]GKS[illegible]DSKLA	S[illegible]IFAQYHE[illegible]	LTSKLSTQNN	FIISKDN-		168
LktC	KGGK[illegible]DKKTA	KKRFDTYQEE	LATALKNEFN	FIKK----		167
ApxIC	HGGKIDKKLA	SKIFQQYHFE	LMSELKNKQN	FKFSLVNS		172
HlyC	HGGKIDKQLA	NKIFKQYHHE	LITEVKNKSD	FNFSLTG-		170

SEQ ID NO: [illegible]
SEQ ID NO: [illegible]
SEQ ID NO: [illegible]
SEQ ID NO: [illegible]

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FIG 12-1

```
    1 ATGTTTATACAAGCACTTAAAGATTTTTTTTATTCGCTATATAACCGTTTGGCGCAATACA   60
    1  M  F  I  Q  A  L  K  D  F     I  R  Y  I  T  V  W  R  N  T

   61 TGGGCAGTTCGAGACCAACTAACCCCTCCTAAGCGTACTAAAGAAGAACTCGCTTTTCTT  120
   21  W  A  V  R  D  Q  L  T  P  P  K  R  T  K  E  E  L  A  F  L   40

  121 CCTGCACATCTAGAACTCACTGACACACCTGTATCCAGATCTTCTAAGTGGACAGCTAGA  180
   41  P  A  H  L  E  L  T  D  T  P  V  S  R  S  S  K  W  T  A  R   60

  181 ATAATCATGATATTTGTCCTATTTGCTTTGCTATGGTCTTGGGTTGGACAGATTGACATT  240
   61  I  I  M  I  F  V  L  F  A  L  L  W  S  W  V  G  Q  I  D  I   80

  241 GTTGCTACAGCTTCAGGTAAAATTTCTTCAGGTAGCCGTAGCAAGACTATTCAATCTTTG  300
   81  V  A  T  A  S  G  K  I  S  S  G  S  R  S  K  T  I  Q  S  L  100

  301 GAAACAGCGATAGTTAAAGCAGTTTATGTACGTGATGGTCAAAATGTTCAACAAGGTGAA  360
  101  E  T  A  I  V  K  A  V  Y  V  R  D  G  Q  N  V  Q  Q  G  E  120

  361 ATATTAGTAGATTTAGTGGGAATCGGTTCAGATAGTGATGTTGCTCAGTCCGAGAAAGCC  420
  121  I  L  V  D  L  V  G  I  G  S  D  S  D  V  A  Q  S  E  K  A  140

  421 CTTCGAGCAGCGCAATTATCTAAGCTACGCCTTGAAGCAATTTTATCAGCATTAAATCAC  480
  141  L  R  A  A  Q  L  S  K  L  R  L  E  A  I  L  S  A  L  N  H  160

  481 CGTATTAATCCTCAGATTGATGTAGCATATGCAAAGTCTTTAAATATTTCAGAATCGGAA  540
  161  R  I  N  P  Q  I  D  V  A  Y  A  K  S  L  N  I  S  E  S  E  180

  541 ATTAATGAAGCTCAAACTTTAGCCCAAAATCAATATCAAGCATGGTTAGCACAAGATGAA  600
  181  I  N  E  A  Q  T  L  A  Q  N  Q  Y  Q  A  W  L  A  Q  D  E  200

  601 CAACTAAAATTAACCTTAAAAGGACATCAAGCAGAATTACAATCTGCTCGATCCCAAGAA  660
  201  Q  L  K  L  T  L  K  G  H  Q  A  E  L  Q  S  A  R  S  Q  E  220

  661 CAAAAGTTGGTTTCAGTTGGTGCAATTGAACATCAAAAGACTGATGATTATCGGAGTCTC  720
  221  Q  K  L  V  S  V  G  A  I  E  H  Q  K  T  D  D  Y  R  S  L  240

  721 AAAGCAGAAAATTTTATATCTGAGCATGCTTATCTAGAACAAGAAAGCAAATTACTTAGC  780
  241  K  A  E  N  F  I  S  E  H  A  Y  L  E  Q  E  S  K  L  L  S  260

  781 AATCAAAATGATTTACAAAGTACACGTAGTCAGATTCAAAAAATACAGGCTGCAATCATG  840
  261  N  Q  N  D  L  Q  S  T  R  S  Q  I  Q  K  I  Q  A  A  I  M  280

  841 CAAGCTGAACAGAACCGTATGTTATATACTCAAAATCTAAAACGTGATACATTAGAATCT  900
  281  Q  A  E  Q  N  R  M  L  Y  T  Q  N  L  K  R  D  T  L  E  S  300

  901 TTACGCCAAACCAATGAACAGATTAATCAATATACTGGTCAAACTAATAAAGCTAAGCAG  960
  301  L  R  Q  T  N  E  Q  I  N  Q  Y  T  G  Q  T  N  K  A  K  Q  320

  961 CGACAGAAATTGCTGAGTATTAAATCACCTGTTAATGGTACTATACAAGAGCTAACAGCT 1020
  321  R  Q  K  L  L  S  I  K  S  P  V  N  G  T  I  Q  E  L  T  A  340

 1021 TATACTTTAGGTGGAGTTGTACAAGCAGCACAAAAAATTATGGTTGTGGCACCTAACGAT 1080
  341  Y  T  L  G  G  V  V  Q  A  A  Q  K  I  M  V  V  A  P  N  D  360

 1081 AATCAAGTGGAAGTAGAGGTATTAGTGCTAAATAAAGATATCGGCTTTGTAAAAGCTGGG 1140
  361  N  Q  V  E  V  E  V  L  V  L  N  K  D  I  G  F  V  K  A  G  380

 1141 CAGAATGTTATCATCAAAATCGAGAGTTTTCCTTATACACGTTATGGTTATTTAACAGGT 1200
  381  Q  N  V  I  I  K  I  E  S  F  P  Y  T  R  Y  G  Y  L  T  G  400

 1201 AAAATAAAAAGTATTAGTCATGATGCTATAGAACATCAACATTTAGGTCTAGTGTATACT 1260
  401  K  I  K  S  I  S  H  D  A  I  E  H  Q  H  L  G  L  V  Y  T  420

 1261 GCACTTGTTTCTCTTGATAAAAGCACATTAAATATAGATGGAGTAACAATCAACTTAACG 1320
  421  A  L  V  S  L  D  K  S  T  L  N  I  D  G  V  T  I  N  L  T  440
```

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```
1321 CCAGGAATGAATGTTACTGCTGAAATTAAAACAGGTAAACGTCGTGTTTTGGATTATATA   1380
 441  P  G  M  N  V  T  A  E  I     T  G  K  R  R  V  L  D  Y  I

1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTTCGAGAACGCTAA               1428
 461  L  S  P  L  Q  T  K  V  D  E  S  F  R  E  R  *                476
```

FIG. 12-2

FIG. 13

MbxD --MF-QALK- FF-RYITVWR NTWA-RDQLT PPKRTK-ELA FLPAHLELT- 48
LktD MKIWLSG-YE PFLRYKN-WA EVWKIRK-LD HPNRKKDESE FLPAHLELIE 50
ApxID MKTWLMGLYE PFQRYKTVWT EIWKIRHQLD TPDREKDENE FLPAHLELIE 50
HlyD MKTWLMGFSE PLLRYKLVWS ETWKIRKQLD TPVREKDENE FLPAHLELIE 50

MbxD TPVSRSS-WT AR-IM-FVLF ALLWSWVGQ- -IVATASGK- SSGSRSKTIQ 98
LktD TPVSKKPRLI AYLIMLFLVV A-VLASVSKV EIVATAPGKL TFSGRSKEIK 100
ApxID TPVSKKPRLI AYLIMLFLFL ALV-SIVSHV EIVATATGKL AFSDRSKEIK 100
HlyD TPVSR-PRL- AYFIMGFLVI AF-LSVLGQV EIVATANGKL TLSGRSKEIK 100

MbxD S-ETAIVKA- -V-DGQNV-Q G--LVDLVG- GSDSDVAQSE KALRAAQLSK 148
LktD PIENAIVQEI FVKDGQFVEK GQLLVSLTAL GSDADIKKTM ASLSLAKLEN 150
ApxID PIENA-VKEI FVQDGQFVEK DQLLLHLTAL GADADQQKTK SSLSLTKLER 150
HlyD PIENSIVKEI IVK-G-SVRK GDVLLKLTAL GA-ADTLKTQ SSLLQA-LEQ 150

MbxD LRLEA-LSA- NHRINPQIDV AYAKSL.NIS ESEINEAQTL AQNQYQAWLA 197
LktD YRYQTLLTAI EKESLPVIDL .SRTEFKDSS EEDRLRIKHL IEEQYTTWQK 199
ApxID YRYEILLEA- AADRLPLI-L .TKDEFKHAT EEDKTRIRYL ITEQFEAWQK 199
HlyD IRYQILSRSI ELNKLPE-KL PDEPYFQNVS EEEVLR-TSL IKEQFSTWQN 200

MbxD QDEQLKLTLK GH-AELQSAR SQEQKLVSVG AIEH-KTDD- RSLKAENFIS 247
LktD QKTQKTLAYK RKEAEKQTIF AY-RKYEGAT RIEQEKLKDF KALYKQKS-S 249
ApxID QKYQKELALQ R-EAEKQT-L ANIRKYEG-S RVENERLKDL KKLFNSKSTS 249
HlyD QKYQKELNLD -KRAE-LTIL ARIN-YENVS RVEKSRLDDF RSLLHKQAIA 250

MbxD EHAYLEQESK L-SNQN-LQS TRSQ-QKI-A AI-QAE-NRM LYTQNLKRDT 297
LktD KHELLAQENK LIEAQNAVAV YRSKLNE-EN DLLNVKEELE LITQFFKSD- 299
ApxID KHDVLTQEN- HIEAVNELAV YKSRLNE-ES DLRQAKEEIH LITQLF-ADI 299
HlyD KHAVLEQENK Y-EAANELRV YKSQLE-IES -ILSAKEEYQ L-TQLFKN-I 300

MbxD LESLRQTNEQ INQYTG-TNK AKQRQKLLSI -SPVNGT-Q- LTA-TLGGVV 347
LktD LEKLKQHIEN ERQLRLELEK NNQRRQASMI RAPVSGTVQQ LKIHTIGGVV 349
ApxID LEKLKQNVEA EKQLSLELEK NEQRQIASVI RAPVSGTVQQ LKTHTVGGVV 349
HlyD L-KLRQTT-S IELLTLELEK NE-RQQASVI RAPVSGKVQQ LKVHTEGGVV 350

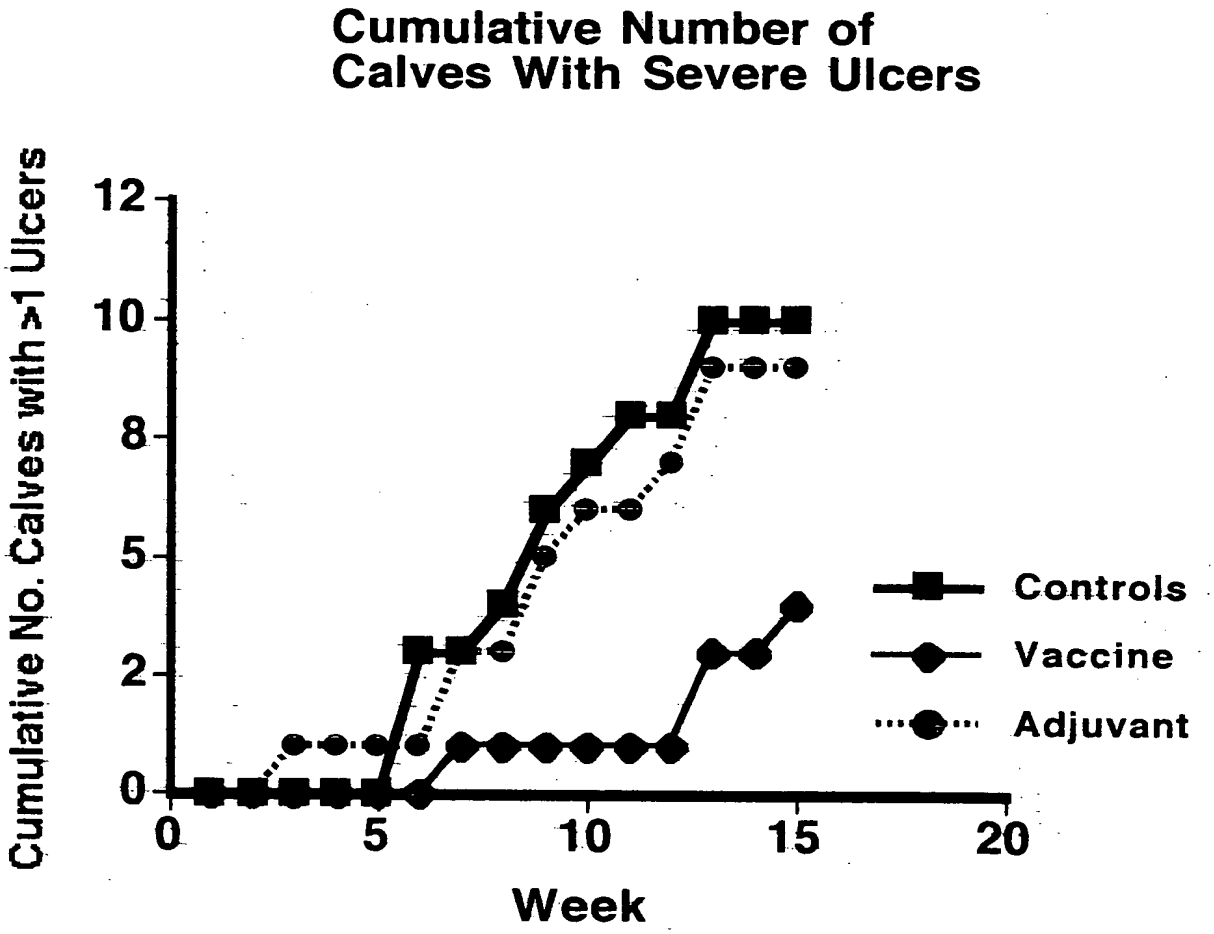
MbxD QAA-K-MV-A PNDNQVEVEV LVLNKDIGFV KAGQNVIIK- ESFPYTRYGY 397
LktD TTAETLM-IV PEDDVLEATA LVPNKDIGFV AAGQEVIIKV ETFPYTRYGY 399
ApxID TTAETLMVIA PEDDVLEVTA L-QNKDIGFI EVGQDA-IKV ETFPYTRYGY 399
HlyD TTAETLMVIV PEDDTLEVTA LVQNKDIGFI NVGQNAIIKV EAFPYTRYGY 400

MbxD LTGKIKSISH DAIEHQHLGL V-TA-VS-D- STLN.IDGVT INLTPGMNVT 446
LktD LTG-IKHISP DAIEQPNVGL VFNATIAIDR KNLTSPDG-K IDLSSGMT-T 449
ApxID LMGKVKNITL -AIEHPQLGL VFNSIISIDR KTLSGKDGKE IELGSGMSVT 449
HlyD LVGKVKNINL DAIEDQKLGL VFNVIVS--E NDLST.GNKH IPLSSGMAVT 449

MbxD AEIKTGKRRV -DY-LSPL-T KVDESFRER 475 SEQ ID NO: 37
LktD AEIKTGERSV MSYLLSPLEE SVTESLRER 478 SEQ ID NO: 38
ApxID AEIKTGERSV ISYLLSPLEE SVSESLRER 478 SEQ ID NO: 39
HlyD AEIKTGMRSV ISYLLSPLEE SVTESLHER 478 SEQ ID NO: 40

09845996 . 100501

FIG. 14



Number of calves with ulcers with clinical scores >+2

F1615

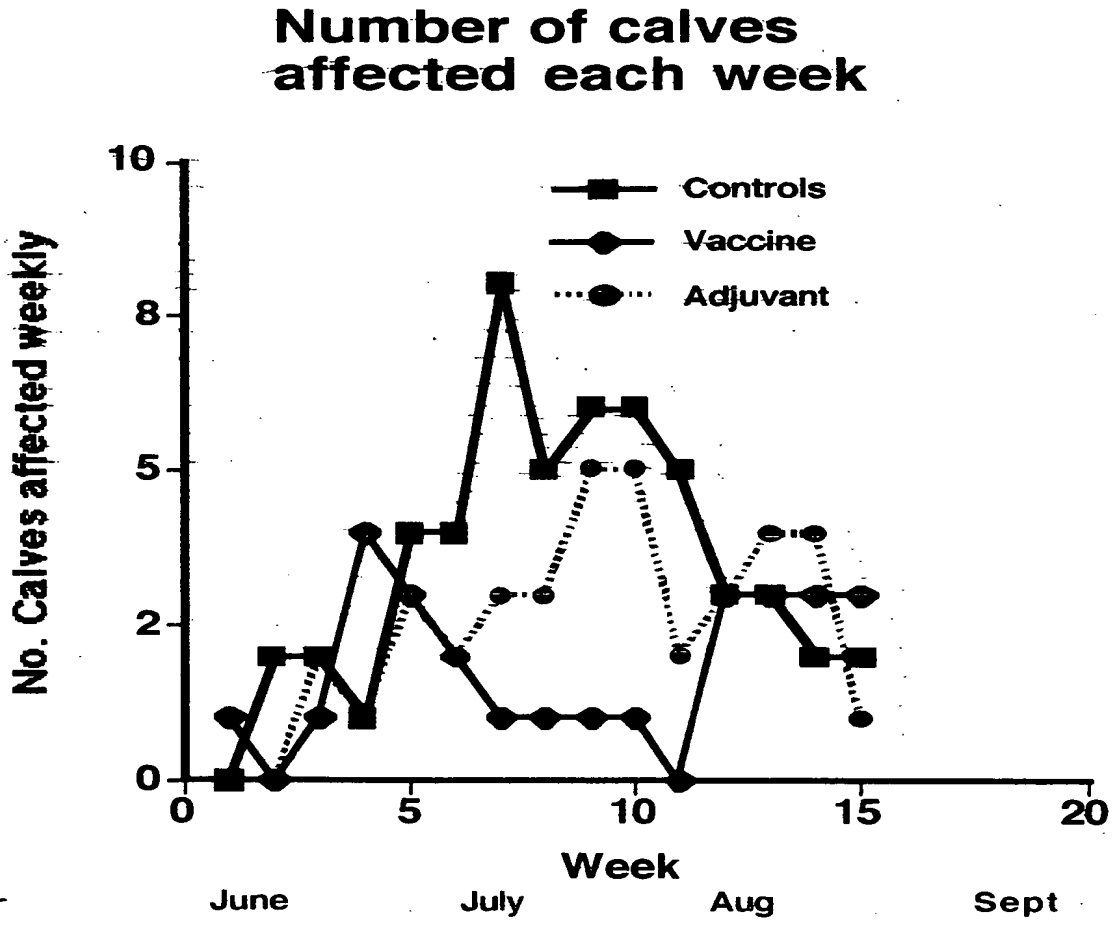
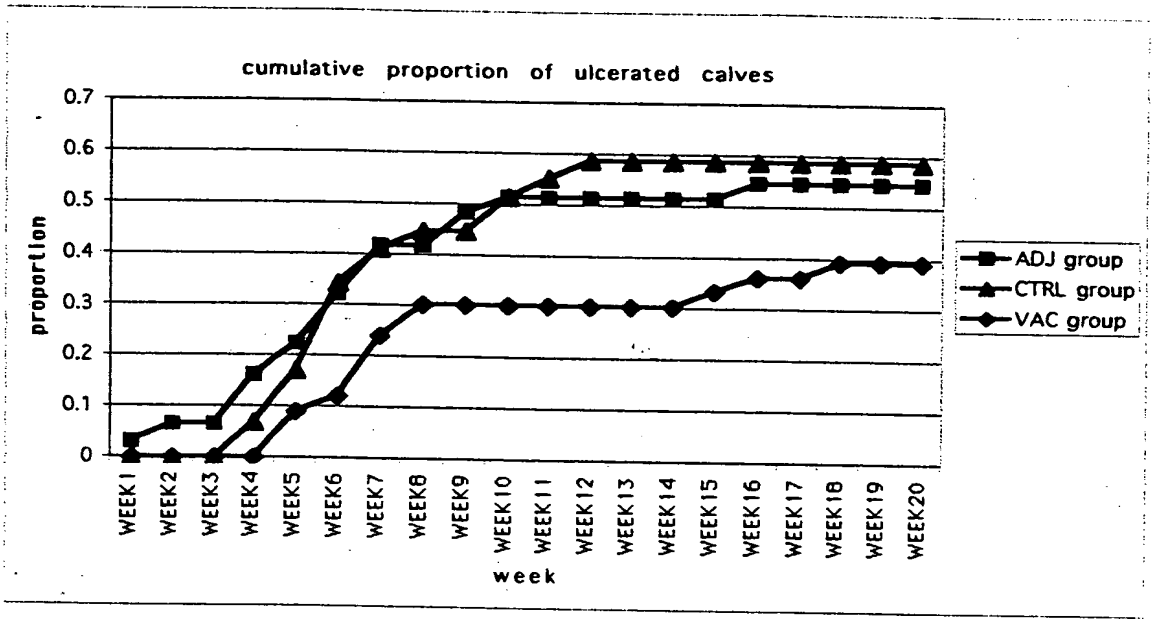


Figure 15
Number of calves affected weekly in 1 group of vaccinated calves and in controls.

FIG. 16



Cumulative proportion of ulcerated calves during the trial. Calves received as vaccines either saline (designated 'CTRL'), adjuvant alone (designated 'ADJ'), or the recombinant cytotoxin vaccine (designated 'VAC').